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Reviewer: markspencer

Timestamp: [year=2012; month=1; day=18; hr=13; min=34; sec=2; ms=40;]

Validated By CRFValidator v 1.0.3

Application No: 08422548 Version No: 2.0

Input Set:

Output Set:

Started: 2012-01-12 15:02:57.842 **Finished:** 2012-01-12 15:02:59.086

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 244 ms

Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 30

Actual SeqID Count: 30

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Eaton, Dan L. $\label{eq:decomposition} \mbox{de Sauvage, Frederic J.}$
- (ii) TITLE OF INVENTION: HUMAN MPL LIGAND
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 460 Point San Bruno Blvd
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08422548
 - (B) FILING DATE: 2012-01-12
 - (A) APPLICATION NUMBER: 08422548
 - (B) FILING DATE: 2012-01-12
 - (C) CLASSIFICATION: 435
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08223263
 - (B) FILING DATE: 1994-04-04
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/08/223, 263A
 - (B) FILING DATE: 04-Apr-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/196689
 - (B) FILING DATE: 15-FEB-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/185607
 - (B) FILING DATE: 21-JAN-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/176553
 - (B) FILING DATE: 3-JAN-1994
- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Winter, Daryl B.
- (B) REGISTRATION NUMBER: 32,637
- (C) REFERENCE/DOCKET NUMBER: P0871P3

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-1249
- (B) TELEFAX: 415/952-9881
- (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr -21 -20 -15 -10

Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu -5 1 5

Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25 30 35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln $40 \hspace{1cm} 45 \hspace{1cm} 50 \hspace{1cm}$

Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu 55 60 65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr 70 75 80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu 85 90 95

Leu Leu Gly Ala Leu Gl
n Ser Leu Leu Gly Thr Gl
n Leu Pro Pro 100 $$105\,$

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr 145 150 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu 160 165 170 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser 175 180 185

Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu 205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn 220 225 230

Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly 235 240 245

Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro 250 255 260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro 265 270 275

Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr 280 285 290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro 295 300 305

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His 310 315 320

Ser Gln Asn Leu Ser Gln Glu Gly 325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100

CCCCACCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150

GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG CTC CTC 239

Met Glu Leu Thr Glu Leu Leu

-21 -20 -15

GTG	GTC	ATG	CTT	CTC	CTA	ACT	GCA	AGG	CTA	ACG	CTG	TCC	278
Val	Val	Met	Leu	Leu	Leu	Thr	Ala	Arg	Leu	Thr	Leu	Ser	
			-10					-5					
AGC	CCG	GCT	CCT	CCT	GCT	TGT	GAC	CTC	CGA	GTC	CTC	AGT	317
Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	
1				5					10				
												CTG	356
Lys		Leu	Arg	Asp	Ser		Val	Leu	His	Ser	_	Leu	
	15					20					25		
7.00	G7.G	maa.	GG 7	G 7 G	GEE E	G7.G	COM	mm.c	COM	3.63	COM	GT.G	205
												GTC	395
ser	GIN	СУЗ		GIU	Val	HIS	Pro		Pro	ınr	Pro	vai	
			30					35					
СТС	СТС	ССТ	ССТ	GTG	GAC	ттт	AGC	TTG	GGA	GAA	TGG	AAA	434
					Asp								101
40	пец	110	AIG	vai	45	THE	Del	пец	Gry	50	пр	шуз	
10					10					30			
ACC	CAG	ATG	GAG	GAG	ACC	AAG	GCA	CAG	GAC	ATT	CTG	GGA	473
					Thr								
		55				_	60		-			65	
GCA	GTG	ACC	CTT	CTG	CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	512
Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	
				70					75				
GGA	CAA	CTG	GGA	CCC	ACT	TGC	CTC	TCA	TCC	CTC	CTG	GGG	551
					ACT Thr								551
													551
	Gln					Cys					Leu		551
Gly	Gln	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90		
Gly CAG	Gln 80 CTT	Leu TCT	Gly GGA Gly	Pro CAG	Thr	Cys 85 CGT	Leu CTC	Ser CTC Leu	Ser CTT	Leu GGG	Leu 90 GCC	Gly CTG	
Gly CAG	Gln 80 CTT	Leu TCT	Gly GGA	Pro CAG	Thr	Cys 85 CGT	Leu CTC	Ser	Ser CTT	Leu GGG	Leu 90 GCC	Gly CTG	
Gly CAG Gln	Gln 80 CTT Leu	Leu TCT Ser	Gly GGA Gly 95	Pro CAG Gln	Thr GTC Val	Cys 85 CGT Arg	Leu CTC Leu	Ser CTC Leu 100	Ser CTT Leu	Leu GGG Gly	Leu 90 GCC Ala	Gly CTG Leu	590
Gly CAG Gln	Gln 80 CTT Leu	TCT Ser	GGA Gly 95 CTT	Pro CAG Gln GGA	Thr GTC Val	Cys 85 CGT Arg	Leu CTC Leu	CTC Leu 100	Ser CTT Leu CCA	Leu GGG Gly CAG	Leu 90 GCC Ala	Gly CTG Leu	590
CAG Gln CAG Gln	Gln 80 CTT Leu	TCT Ser	GGA Gly 95 CTT	Pro CAG Gln GGA	Thr GTC Val ACC Thr	Cys 85 CGT Arg	Leu CTC Leu	CTC Leu 100	Ser CTT Leu CCA	Leu GGG Gly CAG Gln	Leu 90 GCC Ala	Gly CTG Leu	590
Gly CAG Gln	Gln 80 CTT Leu	TCT Ser	GGA Gly 95 CTT	Pro CAG Gln GGA	Thr GTC Val	Cys 85 CGT Arg	Leu CTC Leu	CTC Leu 100	Ser CTT Leu CCA	Leu GGG Gly CAG	Leu 90 GCC Ala	Gly CTG Leu	590
CAG Gln CAG Gln 105	Gln 80 CTT Leu AGC Ser	TCT Ser CTC Leu	GGA Gly 95 CTT Leu	Pro CAG Gln GGA Gly	Thr GTC Val ACC Thr 110	Cys 85 CGT Arg CAG Gln	CTC Leu CTT Leu	CTC Leu 100 CCT Pro	Ser CTT Leu CCA Pro	GGG Gly CAG Gln 115	Leu 90 GCC Ala GGC Gly	Gly CTG Leu AGG Arg	590 629
CAG Gln CAG Gln 105	Gln 80 CTT Leu AGC Ser	TCT Ser CTC Leu	GGA Gly 95 CTT Leu	CAG Gln GGA Gly	GTC Val ACC Thr 110	Cys 85 CGT Arg CAG Gln	CTC Leu CTT Leu	CTC Leu 100 CCT Pro	CTT Leu CCA Pro	GGG Gly CAG Gln 115 TTC	Leu 90 GCC Ala GGC Gly	CTG Leu AGG Arg	590 629
CAG Gln CAG Gln 105	Gln 80 CTT Leu AGC Ser	TCT Ser CTC Leu	GGA Gly 95 CTT Leu	CAG Gln GGA Gly	Thr GTC Val ACC Thr 110	Cys 85 CGT Arg CAG Gln	CTC Leu CTT Leu AAT	CTC Leu 100 CCT Pro	CTT Leu CCA Pro	GGG Gly CAG Gln 115 TTC	Leu 90 GCC Ala GGC Gly	CTG Leu AGG Arg	590 629
CAG Gln CAG Gln 105	Gln 80 CTT Leu AGC Ser	TCT Ser CTC Leu	GGA Gly 95 CTT Leu	CAG Gln GGA Gly	GTC Val ACC Thr 110	Cys 85 CGT Arg CAG Gln	CTC Leu CTT Leu	CTC Leu 100 CCT Pro	CTT Leu CCA Pro	GGG Gly CAG Gln 115 TTC	Leu 90 GCC Ala GGC Gly	CTG Leu AGG Arg	590 629
CAG Gln CAG Gln 105 ACC Thr	Gln 80 CTT Leu AGC Ser	TCT Ser CTC Leu GCT Ala 120	GGA Gly 95 CTT Leu CAC	CAG Gln GGA Gly AAG Lys	GTC Val ACC Thr 110 GAT Asp	Cys 85 CGT Arg CAG Gln	CTC Leu CTT Leu AAT Asn 125	CTC Leu 100 CCT Pro	CTT Leu CCA Pro	GGG Gly CAG Gln 115 TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu	CTG Leu AGG Arg	590 629 668
CAG Gln CAG Gln 105 ACC Thr	Gln 80 CTT Leu AGC Ser ACA Thr	TCT Ser CTC Leu GCT Ala 120	GGA Gly 95 CTT Leu CAC His	CAG Gln GGA Gly AAG Lys	GTC Val ACC Thr 110 GAT Asp	Cys 85 CGT Arg CAG Gln CCC Pro	CTC Leu CTT Leu AAT Asn 125	CTC Leu 100 CCT Pro	CCTT Leu CCA Pro ATC Ile CGT	GGG Gly CAG Gln 115 TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu	CTG Leu AGG Arg AGC Ser 130	590 629 668
CAG Gln CAG Gln 105 ACC Thr	Gln 80 CTT Leu AGC Ser ACA Thr	TCT Ser CTC Leu GCT Ala 120	GGA Gly 95 CTT Leu CAC His	CAG Gln GGA Gly AAG Lys	GTC Val ACC Thr 110 GAT Asp	Cys 85 CGT Arg CAG Gln CCC Pro	CTC Leu CTT Leu AAT Asn 125	CTC Leu 100 CCT Pro	CCTT Leu CCA Pro ATC Ile CGT	GGG Gly CAG Gln 115 TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu	CTG Leu AGG Arg AGC Ser 130	590 629 668
CAG Gln CAG Gln 105 ACC Thr	Gln 80 CTT Leu AGC Ser ACA Thr	TCT Ser CTC Leu GCT Ala 120	GGA Gly 95 CTT Leu CAC His	CAG Gln GGA Gly AAG Lys CTC Leu	GTC Val ACC Thr 110 GAT Asp	Cys 85 CGT Arg CAG Gln CCC Pro	CTC Leu CTT Leu AAT Asn 125	CTC Leu 100 CCT Pro	CCA Pro	GGG Gly CAG Gln 115 TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu	CTG Leu AGG Arg AGC Ser 130	590 629 668
CAG Gln CAG Gln 105 ACC Thr	Gln 80 CTT Leu AGC Ser ACA Thr	TCT Ser CTC Leu GCT Ala 120 CAC	GGA Gly 95 CTT Leu CAC His	CAG Gln GGA Gly AAG Lys CTC Leu 135	GTC Val ACC Thr 110 GAT Asp	Cys 85 CGT Arg CAG Gln CCC Pro	CTC Leu CTT Leu AAT Asn 125 AAG Lys	CTC Leu 100 CCT Pro GCC Ala	CCA Pro ATC Ile CGT Arg 140	GGG Gly CAG Gln 115 TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu CTG Leu	CTG Leu AGG Arg AGC Ser 130 ATG Met	590 629 668
CAG Gln CAG Gln 105 ACC Thr TTC Phe	Gln 80 CTT Leu AGC Ser ACA Thr CAA Gln	TCT Ser CTC Leu GCT Ala 120 CAC His	GGA Gly 95 CTT Leu CAC His CTG Leu	CAG Gln GGA Gly AAG Lys CTC Leu 135	GTC Val ACC Thr 110 GAT Asp	Cys 85 CGT Arg CAG Gln CCC Pro	CTC Leu CTT Leu AAT Asn 125 AAG Lys	CTC Leu 100 CCT Pro GCC Ala GTG Val	CCA Pro ATC Ile CGT Arg 140	GGG Gly CAG Gln 115 TTC Phe TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu CTG Leu	CTG Leu AGG Arg AGC Ser 130 ATG Met	590 629 668
CAG Gln CAG Gln 105 ACC Thr TTC Phe	Gln 80 CTT Leu AGC Ser ACA Thr CAA Gln	TCT Ser CTC Leu GCT Ala 120 CAC His	GGA Gly 95 CTT Leu CAC His CTG Leu	CAG Gln GGA Gly AAG Lys CTC Leu 135	GTC Val ACC Thr 110 GAT Asp CGA Arg	Cys 85 CGT Arg CAG Gln CCC Pro	CTC Leu CTT Leu AAT Asn 125 AAG Lys	CTC Leu 100 CCT Pro GCC Ala GTG Val	CCA Pro ATC Ile CGT Arg 140	GGG Gly CAG Gln 115 TTC Phe TTC Phe	Leu 90 GCC Ala GGC Gly CTG Leu CTG Leu	CTG Leu AGG Arg AGC Ser 130 ATG Met	590 629 668
CAG Gln CAG Gln 105 ACC Thr TTC Phe	Gln 80 CTT Leu AGC Ser ACA Thr CAA Gln GTA Val	TCT Ser CTC Leu GCT Ala 120 CAC His	GGA Gly 95 CTT Leu CAC His CTG Leu	CAG Gln GGA Gly AAG Lys CTC Leu 135	GTC Val ACC Thr 110 GAT Asp CGA Arg	Cys 85 CGT Arg CAG Gln CCC Pro GGA Gly	CTC Leu CTT Leu AAT Asn 125 AAG Lys	CTC Leu 100 CCT Pro GCC Ala GTG Val	CCA Pro ATC Ile CGT Arg 140	GGG Gly CAG Gln 115 TTC Phe TTC Phe	GCC Ala	CTG Leu AGG Arg AGC Ser 130 ATG Met	590 629 668
CAG Gln CAG Gln 105 ACC Thr TTC Phe	Gln 80 CTT Leu AGC Ser ACA Thr CAA Gln GTA Val 145	TCT Ser CTC Leu GCT Ala 120 CAC His	GGA Gly 95 CTT Leu CAC His CTG Leu GGG Gly	CAG Gln GGA Gly AAG Lys CTC Leu 135 TCC Ser	GTC Val ACC Thr 110 GAT Asp CGA Arg ACC Thr	Cys 85 CGT Arg CAG Gln CCC Pro GGA Gly CTC Leu 150	CTC Leu CTT Leu AAT Asn 125 AAG Lys TGC Cys	CTC Leu 100 CCT Pro GCC Ala GTG Val	CCA Pro ATC Ile CGT Arg 140 AGG Arg	GGG Gly CAG Gln 115 TTC Phe CGG Arg	GCC Ala 155	CTG Leu AGG Arg AGC Ser 130 ATG Met	590 629 668 707
CAG Gln CAG Gln 105 ACC Thr TTC Phe CTT Leu CCC	Gln 80 CTT Leu AGC Ser ACA Thr CAA Gln GTA Val 145 ACC	TCT Ser CTC Leu GCT Ala 120 CAC His GGA Gly ACA	GGA Gly 95 CTT Leu CAC His CTG Leu GGG Gly	CAG Gln GGA Gly AAG Lys CTC Leu 135 TCC Ser	GTC Val ACC Thr 110 GAT Asp CGA Arg ACC Thr	Cys 85 CGT Arg CAG Gln CCC Pro GGA Gly CTC Leu 150	CTC Leu CTT Leu AAT Asn 125 AAG Lys TGC Cys	CTC Leu 100 CCT Pro GCC Ala GTG Val GTC Val	CCA Pro ATC Ile CGT Arg 140 AGG Arg	GGG Gly CAG Gln 115 TTC Phe CGG Arg	GCC Ala CTG Leu GCC Ala 155	CTG Leu AGG Arg AGC Ser 130 ATG Met CCA Pro	590 629 668 707

ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 824

Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu 170 175 180

GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 863
Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 902
Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
200 205

CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 941
Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
210 215 220

ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 980

Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn

225

230

GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1019
Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
235 240 245

CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1058
Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
250 255 260

GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1097

Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro

265 270

TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1136

Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe

275 280 285

CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1175

Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
290 295

CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1214

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr

300 305 310

CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253

Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser

315 320 325

CAG AAT CTG TCT CAG GAA GGG T AAGGT TCTCAGACAC 1290
Gln Asn Leu Ser Gln Glu Gly
330 332

CCTGGGAGAC AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC 1390

CCTGGTAAAA GGGATACACA GGACTGAAAA GGGAATCATT TTTCACTGTA 1440

CATTATAAAC	CTTCAGAAGC	TATTTTTTA	AGCTATCAGC	AATACTCATC	1490
AGAGCAGCTA	GCTCTTTGGT	CTATTTTCTG	CAGAAATTTG	CAACTCACTG	1540
ATTCTCTACA	TGCTCTTTTT	CTGTGATAAC	TCTGCAAAGG	CCTGGGCTGG	1590
CCTGGCAGTT	GAACAGAGGG	AGAGACTAAC	CTTGAGTCAG	AAAACAGAGA	1640
AAGGGTAATT	TCCTTTGCTT	CAAATTCAAG	GCCTTCCAAC	GCCCCATCC	1690
CCTTTACTAT	CATTCTCAGT	GGGACTCTGA	TCCCATATTC	TTAACAGATC	1740
TTTACTCTTG	AGAAATGAAT	AAGCTTTCTC	TCAGAAAAA	AAAAAAAAA	1790
AAAAA 1795					

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Val Val Met Leu Leu Thr Ala Arg Leu Thr Leu -16 -15 -10 -5

Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys

1 5 10

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91

Leu Leu Leu Val Val Met Leu

-16 -15 -10

CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130

Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro

-5

CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169 Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg 10 15

GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
20 25 26

CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260
GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310
TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50

TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100

GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150

TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200

GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250

CACAAGCAGG AGGAGCCGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300

AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350

ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu

1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp

35 40 45

Phe	Ser	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Met 55	Glu	Glu	Thr	Lys	Ala 60
Gln	Asp	Ile	Leu	Gly 65	Ala	Val	Thr	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
Ala	Ala	Arg	Gly	Gln 80	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90
Gly	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
Ser	Leu	Leu	Gly	Thr 110	Gln	Leu	Pro	Pro	Gln 115	Gly	Arg	Thr	Thr	Ala 120
His	Lys	Asp	Pro	Asn 125	Ala	Ile	Phe	Leu	Ser 130	Phe	Gln	His	Leu	Leu 135
Arg	Gly	Lys	Val	Arg 140	Phe	Leu	Met	Leu	Val 145	Gly	Gly	Ser	Thr	Leu 150
Cys	Val	Arg	Arg	Ala 155	Pro	Pro	Thr	Thr	Ala 160	Val	Pro	Ser	Arg	Thr 165
Ser	Leu	Val	Leu	Thr 170	Leu	Asn	Glu	Leu	Pro 175	Asn	Arg	Thr	Ser	Gly 180
Leu	Leu	Glu	Thr	Asn 185	Phe	Thr	Ala	Ser	Ala 190	Arg	Thr	Thr	Gly	Ser 195
Gly	Leu	Leu	Lys	Trp 200	Gln	Gln	Gly	Phe	Arg 205	Ala	Lys	Ile	Pro	Gly 210
Leu	Leu	Asn	Gln	Thr 215	Ser	Arg	Ser	Leu	Asp 220	Gln	Ile	Pro	Gly	Tyr 225
Leu	Asn	Arg	Ile	His 230	Glu	Leu	Leu	Asn	Gly 235	Thr	Arg	Gly	Leu	Phe 240
Pro	Gly	Pro	Ser	Arg 245	Arg	Thr	Leu	Gly	Ala 250	Pro	Asp	Ile	Ser	Ser 255
Gly	Thr	Ser	Asp	Thr 260	Gly	Ser	Leu	Pro	Pro 265	Asn	Leu	Gln	Pro	Gly 270
Tyr	Ser	Pro	Ser	Pro 275	Thr	His	Pro	Pro	Thr 280	Gly	Gln	Tyr	Thr	Leu 285
Phe	Pro	Leu	Pro	Pro 290	Thr	Leu	Pro	Thr	Pro 295	Val	Val	Gln	Leu	His 300
Pro	Leu	Leu	Pro	Asp 305	Pro	Ser	Ala	Pro	Thr 310	Pro	Thr	Pro	Thr	Ser 315
Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His	Ser	Gln	Asn	Leu	Ser	Gln

320 325 330

Glu Gly

332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr

1 5 10 15

Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys 35 40 45

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90

Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser 110 115 120

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala 125 130 130

Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg \$140\$ \$145\$ \$150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp \$155\$ 160 165

Arg

166

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

GAG1	CCT	rgg (CCCAC	CCTCT	C TO	CCCAC	CCCGZ	A CTO	CTGC	CGAA	AGA	AGCAC	CAG	50
AAGO	CTCA	AGC (CGCC:	[CCA]	rg go	CCCC	AGGAZ	A AGA	ATTC	AGGG	GAG	AGGCC	CCC	100
ATAC	CAGG	GAG (CCACT	rtca(GT TA	AGACA	ACCC.	I GG(CCAGA	A	Met	GAG Glu -20	143	
CTG	ACT	GAT	TTG	CTC	CTG	GCG	GCC	ATG	CTT	CTT	GCA	GTG	182	
Leu	Thr	Asp	Leu	Leu -15	Leu	Ala	Ala	Met	Leu -10	Leu	Ala	Val		
GCA	AGA	CTA	ACT	CTG	TCC	AGC	CCC	GTA	GCT	CCT	GCC	TGT	221	
Ala	Arg	Leu	Thr	Leu	Ser	Ser	Pro	Val	Ala	Pro	Ala	Суз		
	-5					1				5				
GAC	CCC	AGA	CTC	CTA	AAT	AAA	CTG	CTG	CGT	GAC	TCC	CAC	260	
Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu	Leu	Arg	Asp	Ser	His		
		10					15					20		
CTC	CTT	CAC	AGC	CGA	CTG	AGT	CAG	TGT	CCC	GAC	GTC	GAC	299	
Leu	Leu	His	Ser	Arg	Leu	Ser	Gln	Сув	Pro	Asp	Val	Asp		
				25					30					
CCT	TTG	TCT	ATC	CCT	GTT	CTG	CTG	CCT	GCT	GTG	GAC	TTT	338	
Pro	Leu	Ser	Ile	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe		
	35					40					45			
AGC	CTG	GGA	GAA	TGG	AAA	ACC	CAG	ACG	GAA	CAG	AGC	AAG	377	
Ser	Leu	Gly		Trp	Lys	Thr	Gln		Glu	Gln	Ser	Lys		
			50					55						
												GAG	416	
	Gln	Asp	Ile	Leu		Ala	Val	Ser	Leu		Leu	Glu		
60					65					70				
GGA	GTG	ATG	GCA	GCA	CGA	GGA	CAG	TTG	GAA	CCC	TCC	TGC	455	
Gly	Val		Ala	Ala	Arg	Gly		Leu	Glu	Pro	Ser	_		
		75					80					85		
CTC	TCA	TCC	CTC	CTG	GGA	CAG	CTT	TCT	GGG	CAG	GTT	CGC	494	
Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	_	Gln	Val	Arg		
				90					95					
CTC	CTC	TTG	GGG	GCC	CTG	CAG	GGC	CTC	CTA	GGA	ACC	CAG	533	
Leu	Leu	Leu	Gly	Ala	Leu	Gln	Gly	Leu	Leu	Gly	Thr	Gln		
	100					105					110			

TTG AGC TTG CAA CAA CTG CTT CGG GGA AAG GTG CGC TTC 611

GGC AGG ACC ACA GCT CAC AAG GAC CCC AAT GCC CTC TTC 572 Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe

120

115

Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe 125 130 135